

SEQUENCE LISTING

5 (1) GENERAL INFORMATION:

(i) APPLICANTS: Morrow, Casey D. and Porter, Donna, C.

10 (ii) TITLE OF INVENTION: ENCAPSIDATED RECOMBINANT POLIOVIRUS
NUCLEIC ACID AND METHODS OF MAKING AND
USING SAME

(iii) NUMBER OF SEQUENCES: 23

15 (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD
(B) STREET: 60 STATE STREET, SUITE 510
(C) CITY: BOSTON
20 (D) STATE: MASSACHUSETTS
(E) COUNTRY: USA
(F) ZIP: 02109

25 (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
30 (D) SOFTWARE: ASCII

35 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 000000
(B) FILING DATE: 15-FEB-1995
(C) CLASSIFICATION:

40 (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/087,009
(B) FILING DATE: 01-JUL-1993
(C) CLASSIFICATION:

45 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Silveri, Jean M.
(B) REGISTRATION NUMBER: P-39,030
(C) REFERENCE/DOCKET NUMBER: UAG-004CP

50 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 227-7400
(B) TELEFAX: (617) 227-5941

55 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
55 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

5 TATTAGTAGA TCTG

14

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

20 TACAGATGTA CTAA

14

(2) INFORMATION FOR SEQ ID NO:3:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 846 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: cDNA

35 (ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 20..845

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

40 ACACAGCAAT CAGGTCAGC CAA AAT TAC CCT ATA GTG CAG AAC ATC CAG GGG 52
Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly
1 5 10

45 CAA ATG GTA CAT CAG GCC ATA TCA CCT AGA ACT TTA AAT GCA TGG GTA 100
Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val
15 20 25

50 AAA GTA GTA GAA GAG AAG GCT TTC AGC CCA GAA GTG ATA CCC ATG TTT 148
Lys Val Val Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe
30 35 40

55 TCA GCA TTA TCA GAA GGA GCC ACC CCA CAA GAT TTA AAC ACC ATG CTA 196
Ser Ala Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu
45 50 55

	AAC ACA GTG GGG GGA CAT CAA GCA GCC ATG CAA ATG TTA AAA GAG ACC		244
	Asn Thr Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr		
60	65	70	75
5	ATC AAT GAG GAA GCT GCA GAA TGG GAT AGA GTG CAT CCA GTG CAT GCA		292
	Ile Asn Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala		
	80	85	90
10	GGG CCT ATT GCA CCA GGC CAG ATG AGA GAA CCA AGG GGA AGT GAC ATA		340
	Gly Pro Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile		
	95	100	105
15	GCA GGA ACT ACT AGT ACC CTT CAG GAA CAA ATA GGA TGG ATG ACA AAT		388
	Ala Gly Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn		
	110	115	120
20	AAT CCA CCT ATC CCA GTA GGA GAA ATT TAT AAA AGA TGG ATA ATC CTG		436
	Asn Pro Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu		
	125	130	135
25	GGA TTA AAT AAA ATA GTA AGA ATG TAT AGC CCT ACC AGC ATT CTG GAC		484
	Gly Leu Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp		
	140	145	150
30	ATA AGA CAA GGA CCA AAG GAA CCC TTT AGA GAC TAT GTA GAC CGG TTC		532
	Ile Arg Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe		
	160	165	170
35	TAT AAA ACT CTA AGA GCC GAG CAA GCT TCA CAG GAG GTA AAA AAT TGG		580
	Tyr Lys Thr Leu Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp		
	175	180	185
40	ATG ACA GAA ACC TTG TTG GTC CAA AAT GCG AAC CCA GAT TGT AAG ACT		628
	Met Thr Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr		
	190	195	200
45	ATT TTA AAA GCA TTG GGA CCA GCG GCT ACA CTA GAA GAA ATG ATG ACA		676
	Ile Leu Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr		
	205	210	215
50	GCA TGT CAG GGA GTA GGA CCC GGC CAT AAG GCA AGA GTT TTG GCT		724
	Ala Cys Gln Gly Val Gly Pro Gly His Lys Ala Arg Val Leu Ala		
	220	225	230
55	GAA GCA ATG AGC CAA GTA ACA AAT TCA GCT ACC ATA ATG ATG CAG AGA		772
	Glu Ala Met Ser Gln Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg		
	240	245	250
55	AAA GAA GGG CAC ACA GCC AGA AAG T		846
	Lys Glu Gly His Thr Ala Arg Lys		
	270	275	

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

5 (A) LENGTH: 275 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His Gln
1 5 10 15

15 Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu Glu
20 25 30

Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser Glu
35 40 45

20 Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly Gly
50 55 60

25 His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu Ala
65 70 75 80

30 Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala Pro
85 90 95

35 Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr Ser
100 105 110

40 Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile Pro
115 120 125

45 Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile
130 135 140

50 Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly Pro
145 150 155 160

Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu Arg
165 170 175

55 Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr Leu
180 185 190

Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala Leu
195 200 205

50 Gly Pro Ala Ala Thr Leu Glu Met Met Thr Ala Cys Gln Gly Val
210 215 220

55 Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser Gln
225 230 235 240

Val Thr Asn Ser Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg Asn
245 250 255

Gln Arg Lys Ile Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His Thr
260 265 270

5 Ala Arg Lys
275

(2) INFORMATION FOR SEQ ID NO:5:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 948 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

20 (A) NAME/KEY: CDS
(B) LOCATION: 4..946

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

25 AAC CAA TGG CCA TTG ACA GAA GAA AAA ATA AAA GCA TTA GTA GAA ATT
Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile
1 5 10 15

48

30 TGT ACA GAG ATG GAA AAG GAA GGG AAA ATT TCA AAA ATT GGG CCT GAA
Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu
20 25 30

96

35 AAT CCA TAC AAT ACT CCA GTA TTT GCC ATA AAG AAA AAA GAC AGT ACT
Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr
35 40 45

144

40 AAA TGG AGA AAA TTA GTA GAT TTC AGA GAA CTT AAT AAG AGA ACT CAA
Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln
50 55 60

192

45 GAC TTC TGG GAA GTT CAA TTA GGA ATA CCA CAT CCC GCA GGG TTA AAA
Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys
65 70 75

240

50 AAG AAA AAA TCA GTA ACA GTA CTG GAT GTG GGT GAT GCA TAT TTT TCA
Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser
80 85 90 95

288

55 GTT CCC TTA GAT GAA GAC TTC AGG AAG TAT ACT GCA TTT ACC ATA CCT
Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro
100 105 110

336

AGT ATA AAC AAT GAG ACA CCA GGG ATT AGA TAT CAG TAC AAT GTG CTT
Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu
115 120 125

384

CCA CAG GGA TGG AAA GGA TCA CCA GCA ATA TTC CAA AGT AGC ATG ACA	432
Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr	
130 135 140	
5 AAA ATC TTA GAG CCT TTT AGA AAA CAA AAT CCA GAC ATA GTT ATC TAT	480
Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr	
145 150 155	
10 CAA TAC ATG GAT GAT TTG TAT GTA GGA TCT GAC TTA GAA ATA GGG CAG	528
Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln	
160 165 170 175	
15 CAT AGA ACA AAA ATA GAG GAG CTG AGA CAA CAT CTG TTG AGG TGG GGA	576
His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly	
180 185 190	
20 CTT ACC ACA CCA GAC AAA AAA CAT CAG AAA GAA CCT CCA TTC CTT TGG	624
Leu Thr Thr Pro Asp Lys His Gln Lys Glu Pro Pro Phe Leu Trp	
195 200 205	
25 ATG GGT TAT GAA CTC CAT CCT GAT AAA TGG ACA GTA CAG CCT ATA GTG	672
Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Val	
210 215 220	
30 CTG CCA GAA AAA GAC AGC TGG ACT GTC AAT GAC ATA CAG AAG TTA GTG	720
Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val	
225 230 235	
35 GGG AAA TTG AAT TGG GCA AGT CAG ATT TAC CCA GGG ATT AAA GTA AGG	768
Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Pro Gly Ile Lys Val Arg	
240 245 250 255	
40 CAA TTA TGT AAA CTC CTT AGA GGA ACC AAA GCA CTA ACA GAA GTA ATA	816
Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile	
260 265 270	
45 CCA CTA ACA GAA GAA GCA GAG CTA GAA CTG GCA GAA AAC AGA GAG ATT	864
Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile	
275 280 285	
50 CTA AAA GAA CCA GTA CAT GGA GTG TAT TAT GAC CCA TCA AAA GAC TTA	912
Leu Lys Glu Pro Val His Gly Val Tyr Tyr Asp Pro Ser Lys Asp Leu	
290 295 300	
45 ATA GCA GAA ATA CAG AAG CAG GGG CAA GGC CTCGAG	948
Ile Ala Glu Ile Gln Lys Gln Gly Gln Gly	
305 310	

50 (2) INFORMATION FOR SEQ ID NO:6:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

5 Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile Cys
1 5 10 15

10 Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu Asn
20 25 30

15 Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr Lys
35 40 45

20 Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln Asp
50 55 60

25 Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys Lys
65 70 75 80

30 Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser Val
85 90 95

35 Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro Ser
100 105 110

40 Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu Pro
115 120 125

45 Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr Lys
130 135 140

50 Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr Gln
145 150 155 160

55 Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln His
165 170 175

60 Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly Leu
180 185 190

65 Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp Met
195 200 205

70 Gly Tyr Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Val Leu
210 215 220

75 Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val Gly
225 230 235 240

80 Lys Leu Asn Trp Ala Ser Gln Ile Tyr Pro Gly Ile Lys Val Arg Gln
245 250 255

85 Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile Pro
260 265 270

90 Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile Leu
275 280 285

Lys Glu Pro Val His Gly Val Tyr Tyr Asp Pro Ser Lys Asp Leu Ile
290 295 300

5 Ala Glu Ile Gln Lys Gln Gly Gln Gly Leu
305 310

(2) INFORMATION FOR SEQ ID NO:7:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1568 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

20 (A) NAME/KEY: CDS
(B) LOCATION: 7..1565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

25 GGGGCC TGT CCA AAG GTA TCC TTT GAG CCA ATT CCC ATA CAT TAT TGT
Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys
1 5 10

48

30 GCC CCG GCT GGT TTT GCG ATT CTA AAA TGT AAT AAT AAG ACG TTC AAT
Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn
15 20 25 30

96

35 GGA ACA GGA CCA TGT ACA AAT GTC AGC ACA GTA CAA TGT ACA CAT GGA
Gly Thr Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly
35 40 45

144

40 ATT AGG CCA GTA GTA TCA ACT CAA CTG CTG TTA AAT GGC AGT CTA GCA
Ile Arg Pro Val Val Ser Thr Gln Leu Leu Asn Gly Ser Leu Ala
50 55 60

192

45 GAA GAA GAG GTA ATT AGA TCT GTC AAT TTC ACG GAC AAT GCT AAA
Glu Glu Val Val Ile Arg Ser Val Asn Phe Thr Asp Asn Ala Lys
65 70 75

240

50 ACC ATA ATA GTA CAG CTG AAC ACA TCT GTA GAA ATT AAT TGT ACA AGA
Thr Ile Ile Val Gln Leu Asn Thr Ser Val Glu Ile Asn Cys Thr Arg
80 85 90

288

55 CCC AAC AAC AAT ACA AGA AAA AGA ATC CGT ATC CAG AGA GGA CCA GGG
Pro Asn Asn Asn Thr Arg Lys Arg Ile Arg Ile Gln Arg Gly Pro Gly
95 100 105 110

336

AGA GCA TTT GTT ACA ATA GGA AAA ATA GGA AAT ATG AGA CAA GCA CAT
Arg Ala Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His
115 120 125

384

5	TGT AAC ATT AGT AGA GCA AAA TGG AAT AAC ACT TTA AAA CAG ATA GAT Cys Asn Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Lys Gln Ile Asp 130 135 140	432
10	AGC AAA TTA AGA GAA CAA TTC GGA AAT AAT AAA ACA ATA ATC TTT AAG Ser Lys Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys 145 150 155	480
15	CAA TCC TCA GGA GGG GAC CCA GAA ATT GTA ACG CAC AGT TTT AAT TGT Gln Ser Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys 160 165 170	528
20	GGA GGG GAA TTT TTC TAC TGT AAT TCA ACA CAA CTG TTT AAT AGT ACT Gly Gly Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr 175 180 185 190	576
25	TGG TTT AAT AGT ACT TGG AGT ACT GAA GGG TCA AAT AAC ACT GAA GGA Trp Phe Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly 195 200 205	624
30	AGT GAC ACA ATC ACC CTC CCA TGC AGA ATA AAA CAA ATT ATA AAC ATG Ser Asp Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met 210 215 220	672
35	TGG CAG AAA GTA GGA AAA GCA ATG TAT GCC CCT CCC ATC AGT GGA CAA Trp Gln Lys Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln 225 230 235	720
40	ATT AGA TGT TCA TCA AAT ATT ACA GGG CTG CTA TTA ACA AGA GAT GGT Ile Arg Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly 240 245 250	768
45	GGT AAT AGC AAC AAT GAG TCC GAG ATC TTC AGA CTT GGA GGA GAT Gly Asn Ser Asn Asn Glu Ser Glu Ile Phe Arg Leu Gly Gly Asp 255 260 265 270	816
50	ATG AGG GAC AAT TGG AGA AGT GAA TTA TAT AAA TAT AAA GTC GTC AAA Met Arg Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys 275 280 285	864
55	ATT GAA CCA TTA GGA GTA GCA CCC ACC AAG GCA AAG AGA AGA GTG GTG Ile Glu Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val 290 295 300	912
60	CAG AGA GAA AAA AGA GCA GTG GGA ATA GGA GCT TTG TTC CTT GGG TTC Gln Arg Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe 305 310 315	960
65	TTG GGA GCA GCA GGA AGC ACT ATG GGC GCA GCC TCA ATG ACG CTG ACG Leu Gly Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr 320 325 330	1008
70	GTA CAG GCC AGA CAA TTA TTG TCT GGT ATA GTG CAG CAG CAG AAC AAT Val Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn 335 340 345 350	1056

TTG CTG AGG GCT ATT GAG GCG CAA CAG CAT CTG TTG CAA CTC ACA GTC	1104
Leu Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val	
355 360 365	
5 TGG GGC ATC AAG CAG CTC CAA GCA AGA ATC CTA GCT GTG GAA AGA TAC	1152
Trp Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr	
370 375 380	
10 CTA AAG GAT CAA CAG CTC CTA GGG ATT TGG GGT TGC TCT GGA AAA CTC	1200
Leu Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu	
385 390 395	
15 ATT TGC ACC ACT GCT GTG CCT TGG AAT GCT AGT TGG AGT AAT AAA TCT	1248
Ile Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser	
400 405 410	
20 CTG GAA CAG ATC TGG AAT CAC ACG ACC TGG ATG GAG TGG GAC AGA GAA	1296
Leu Glu Gln Ile Trp Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu	
415 420 425 430	
25 ATT AAC AAT TAC ACA AGC TTA ATA CAC TCC TTA ATT GAA GAA TCG CAA	1344
Ile Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln	
435 440 445	
30 AAC CAG CAA GAA AAG AAT GAA CAA GAA TTA TTG GAA TTA GAT AAA TGG	1392
Asn Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp	
450 455 460	
35 GCA AGT TTG TGG AAT TGG TTT AAC ATA ACA AAT TGG CTG TGG TAT ATA	1440
Ala Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile	
465 470 475	
40 AAA TTA TTC ATA ATG ATA GTA GGA GGC TTG GTA GGT TTA AGA ATA GTT	1488
Lys Leu Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val	
480 485 490	
45 TTT GCT GTA CTT TCT ATA GTG AAT AGA GTT AGG CAG GGA TAT TCA CCA	1536
Phe Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro	
495 500 505 510	
50 TTA TCG TTT CAG ACC CAC CTC CCA ATC TCGAG	1568
Leu Ser Phe Gln Thr His Leu Pro Ile	
515	

45 (2) INFORMATION FOR SEQ ID NO:8:

50 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

5 Cys Pro Lys Val Ser Phe Glu Pro Ile Pro Ile His Tyr Cys Ala Pro
1 5 10 15

Ala Gly Phe Ala Ile Leu Lys Cys Asn Asn Lys Thr Phe Asn Gly Thr
20 25 30

10 Gly Pro Cys Thr Asn Val Ser Thr Val Gln Cys Thr His Gly Ile Arg
35 40 45

Pro Val Val Ser Thr Gln Leu Leu Asn Gly Ser Leu Ala Glu Glu
50 55 60

15 Glu Val Val Ile Arg Ser Val Asn Phe Thr Asp Asn Ala Lys Thr Ile
65 70 75 80

20 Ile Val Gln Leu Asn Thr Ser Val Glu Ile Asn Cys Thr Arg Pro Asn
85 90 95

Asn Asn Thr Arg Lys Arg Ile Arg Ile Gln Arg Gly Pro Gly Arg Ala
100 105 110

25 Phe Val Thr Ile Gly Lys Ile Gly Asn Met Arg Gln Ala His Cys Asn
115 120 125

Ile Ser Arg Ala Lys Trp Asn Asn Thr Leu Lys Gln Ile Asp Ser Lys
130 135 140

30 Leu Arg Glu Gln Phe Gly Asn Asn Lys Thr Ile Ile Phe Lys Gln Ser
145 150 155 160

35 Ser Gly Gly Asp Pro Glu Ile Val Thr His Ser Phe Asn Cys Gly Gly
165 170 175

Glu Phe Phe Tyr Cys Asn Ser Thr Gln Leu Phe Asn Ser Thr Trp Phe
180 185 190

40 Asn Ser Thr Trp Ser Thr Glu Gly Ser Asn Asn Thr Glu Gly Ser Asp
195 200 205

Thr Ile Thr Leu Pro Cys Arg Ile Lys Gln Ile Ile Asn Met Trp Gln
210 215 220

45 Lys Val Gly Lys Ala Met Tyr Ala Pro Pro Ile Ser Gly Gln Ile Arg
225 230 235 240

50 Cys Ser Ser Asn Ile Thr Gly Leu Leu Leu Thr Arg Asp Gly Gly Asn
245 250 255

Ser Asn Asn Glu Ser Glu Ile Phe Arg Leu Gly Gly Asp Met Arg
260 265 270

55 Asp Asn Trp Arg Ser Glu Leu Tyr Lys Tyr Lys Val Val Lys Ile Glu
275 280 285

Pro Leu Gly Val Ala Pro Thr Lys Ala Lys Arg Arg Val Val Gln Arg
 290 295 300

5 Glu Lys Arg Ala Val Gly Ile Gly Ala Leu Phe Leu Gly Phe Leu Gly
 305 310 315 320

Ala Ala Gly Ser Thr Met Gly Ala Ala Ser Met Thr Leu Thr Val Gln
 325 330 335

10 Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Asn Asn Leu Leu
 340 345 350

15 Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly
 355 360 365

Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu Lys
 370 375 380

20 Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys
 385 390 395 400

Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Glu
 405 410 415

25 Gln Ile Trp Asn His Thr Thr Trp Met Glu Trp Asp Arg Glu Ile Asn
 420 425 430

30 Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn Gln
 435 440 445

Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser
 450 455 460

35 Leu Trp Asp Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys Leu
 465 470 475 480

Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala
 485 490 495

40 Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser
 500 505 510

Phe Gln Thr His Leu Pro Ile
 45 515

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CACCCCTCTC CTACGTAACC AAGGATC

27

5 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTACTGGTCA CCATATTGGT CAAC

24

20 (2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

35 GGAGAGAGAT GGGAGCTCGA GCGTC

25

(2) INFORMATION FOR SEQ ID NO:12:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: cDNA

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

55 GCCCCCCCTAT ACGTATTGTG

20

(2) INFORMATION FOR SEQ ID NO:13:

55 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

10 CCAGTGAAATT CCTAATACGA CTCACTATAG GTTAAAACAG C

41

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

15

20 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

25 CTCTATCCTG AGCTCCATAT GTGTCGAGCA GTTTTGTT TAGCATTG

48

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

30

35 (ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Lys Asp Leu Thr Thr Tyr Gly
1 5

45 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: cDNA

55

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5	CGA CCA GCA GAC CAG ACA GTC ACA GCA GCC TTG ACA AAA CGT TCC TGG	48		
	Arg Pro Ala Asp Gln Thr Val Thr Ala Ala Leu Thr Lys Arg Ser Trp			
1	5	10	15	
10	AAC TCA AGC ACT TCT CCA CAG AGG AGG ACA GAG CAG ACA GCA GAG ACC	96		
	Asn Ser Ser Thr Ser Pro Gln Arg Arg Thr Glu Gln Thr Ala Glu Thr			
	20	25	30	
15	ATG GAG TCT CCC TCG GCC CCT CCC CAC AGA TGG TGC ATC CCC TGG CAG	144		
	Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln			
	35	40	45	
20	AGG CTC CTG CTC ACA GCC TCA CTT CTA ACC TTC TGG AAC CCG CCC ACC	192		
	Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr			
	50	55	60	
25	ACT GCC AAG CTC ACT ATT GAA TCC ACG CCG TTC AAT GTC GCA GAG GGG	240		
	Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly			
	65	70	75	80
30	AAG GAG GTG CTT CTA CTT GTC CAC AAT CTG CCC CAG CAT CTT TTT GGC	288		
	Lys Glu Val Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly			
	85	90	95	
35	TAC AGC TGG TAC AAA GGT GAA AGA GTG GAT GGC AAC CGT CAA ATT ATA	336		
	Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile			
	100	105	110	
40	GGA TAT GTA ATA GGA ACT CAA CAA GCT ACC CCA GGG CCC GCA TAC AGT	384		
	Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser			
	115	120	125	
45	GGT CGA GAG ATA ATA TAC CCC AAT GCA TCC CTG CTG ATC CAG AAC ATC	432		
	Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile			
	130	135	140	
50	ATC CAG AAT GAC ACA GGA TTC TAC ACC CTA CAC GTC ATA AAG TCA GAT	480		
	Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp			
	145	150	155	160
55	CTT GTG AAT GAA GAA GCA ACT GGC CAG TTC CGG GTA TAC CCG GAG CTG	528		
	Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu			
	165	170	175	
60	CCC AAG CCC TCC ATC TCC AGC AAC AAC TCC AAA CCC GTG GAG GAC AAG	576		
	Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys			
	180	185	190	
65	GAT GCT GTG GCC TTC ACC TGT GAA CCT GAG ACT CAG GAC GCA ACC TAC	624		
	Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr			
	195	200	205	
70	CTG TGG TGG GTA AAC AAT CAG AGC CTC CCG GTC AGT CCC AGG CTG CAG	672		
	Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln			

210

215

220

5	CTG TCC AAT GGC AAC AGG ACC CTC ACT CTA TTC AAT GTC ACA AGA AAT Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn 225 230 235 240	720
10	GAC ACA GCA AGC TAC AAA TGT GAA ACC CAG AAC CCA GTG AGT GCC AGG Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg 245 250 255	768
15	CGC AGT GAT TCA GTC ATC CTG AAT GTC CTC TAT GGC CCG GAT GCC CCC Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro 260 265 270	816
20	ACC ATT TCC CCT CTA AAC ACA TCT TAC AGA TCA GGG GAA AAT CTG AAC Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn 275 280 285	864
25	CTC TCC TGC CAT GCA GCC TCT AAC CCA CCT GCA CAG TAC TCT TGG TTT Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe 290 295 300	912
30	GTC AAT GGG ACT TTC CAG CAA TCC ACC CAA GAG CTC TTT ATC CCC AAC Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn 305 310 315 320	960
35	ATC ACT GTG AAT AAT AGT GGA TCC TAT ACG TGC CAA GCC CAT AAC TCA Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser 325 330 335	1008
40	GAC ACT GGC CTC AAT AGG ACC ACA GTC ACG ACG ATC ACA GTC TAT GCA Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Ile Thr Val Tyr Ala 340 345 350	1056
45	GAG CCA CCC AAA CCC TTC ATC ACC AGC AAC AAC TCC AAC CCC GTG GAG Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu 355 360 365	1104
50	GAT GAG GAT GCT GTA GCC TTA ACC TGT GAA CCT GAG ATT CAG AAC ACA Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr 370 375 380	1152
55	ACC TAC CTG TGG TGG GTA AAT AAT CAG AGC CTC CCG GTC AGT CCC AGG Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg 385 390 395 400	1200
55	CTG CAG CTG TCC AAT GAC AAC AGG ACC CTC ACT CTA CTC AGT GTC ACA Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr 405 410 415	1248
55	AGG AAT GAT GTA GGA CCC TAT GAG TGT GGA ATC CAG AAC GAA TTA AGT Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser 420 425 430	1296
55	GTT GAC CAC AGC GAC CCA GTC ATC CTG AAT GTC CTC TAT GGC CCA GAC Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp 435 440 445	1344

	GAC CCC ACC ATT TCC CCC TCA TAC ACC TAT TAC CGT CCA GGG GTG AAC	1392
	Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn	
	450 455 460	
5	CTC AGC CTC TCC TGC CAT GCA GCC TCT AAC CCA CCT GCA CAG TAT TCT	1440
	Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser	
	465 470 475 480	
10	TGG CTG ATT GAT GGG AAC ATC CAG CAA CAC ACA CAA GAG CTC TTT ATC	1488
	Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile	
	485 490 495	
15	TCC AAC ATC ACT GAG AAG AAC AGC GGA CTC TAT ACC TGC CAG GCC AAT	1536
	Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn	
	500 505 510	
20	AAC TCA GCC AGT GGC CAC AGC AGG ACT ACA GTC AAG ACA ATC ACA GTC	1584
	Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val	
	515 520 525	
25	TCT GCG GAG CTG CCC AAG CCC TCC ATC TCC AGC AAC AAC TCC AAA CCC	1632
	Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro	
	530 535 540	
30	GTG GAG GAC AAG GAT GCT GTG GCC TTC ACC TGT GAA CCT GAG GCT CAG	1680
	Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln	
	545 550 555 560	
35	AAC ACA ACC TAC CTG TGG TGG GTA AAT GGT CAG AGC CTC CCA GTC AGT	1728
	Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser	
	565 570 575	
40	CCC AGG CTG CAG CTG TCC AAT GGC AAC AGG ACC CTC ACT CTA TTC AAT	1776
	Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn	
	580 585 590	
45	GTC ACA AGA AAT GAC GCA AGA GCC TAT GTA TGT GGA ATC CAG AAC TCA	1824
	Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser	
	595 600 605	
50	GTG AGT GCA AAC CGC AGT GAC CCA GTC ACC CTG GAT GTC CTC TAT GGG	1872
	Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly	
	610 615 620	
55	GTG AGT GCA AAC CGC AGT GAC CCA GTC ACC CTG GAT GTC CTC TAT GGG	1920
	Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly	
	625 630 635 640	
60	GCG AAC CTC AAC CTC TCC TGC CAC TCG GCC TCT AAC CCA TCC CCG CAG	1968
	Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln	
	645 650 655	
65	TAT TCT TGG CGT ATC AAT GGG ATA CCG CAG CAA CAC ACA CAA GTT CTC	2016
	Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu	
	660 665 670	

TTT ATC GCC AAA ATC ACG CCA AAT AAT AAC GGG ACC TAT GCC TGT TTT Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe 675 680 685	2064
5 GTC TCT AAC TTG GCT ACT GGC CGC AAT AAT TCC ATA GTC AAG AGC ATC Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile 690 695 700	2112
10 ACA GTC TCT GCA TCT GGA ACT TCT CCT GGT CTC TCA GCT GGG GCC ACT Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr 705 710 715 720	2160
15 GTC GGC ATC ATG ATT GGA GTG CTG GTT GGG GTT GCT CTG ATA Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile 725 730	2202
20 TAGCAGCCCT GGTGTAGT	2220
20 (2) INFORMATION FOR SEQ ID NO:17:	
25 (i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 734 amino acids	
(B) TYPE: amino acid	
(D) TOPOLOGY: linear	
30 (ii) MOLECULE TYPE: protein	
35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
Arg Pro Ala Asp Gln Thr Val Thr Ala Ala Leu Thr Lys Arg Ser Trp 1 5 10 15	
Asn Ser Ser Thr Ser Pro Gln Arg Arg Thr Glu Gln Thr Ala Glu Thr 20 25 30	
Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln 35 40 45	
40 Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr 50 55 60	
45 Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly 65 70 75 80	
Lys Glu Val Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly 85 90 95	
50 Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile 100 105 110	
Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser 115 120 125	
55 Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile 130 135 140	

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
145 150 155 160

5 Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
165 170 175

Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
180 185 190

10 Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
195 200 205

Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg Leu Gln
15 210 215 220

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
225 230 235 240

20 Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
245 250 255

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
260 265 270

25 Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
275 280 285

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
30 290 295 300

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
305 310 315 320

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
35 325 330 335

Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
340 345 350

40 Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
355 360 365

Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
45 370 375 380

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
385 390 395 400

Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu Ser Val Thr
50 405 410 415

Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn Glu Leu Ser
420 425 430

55 Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr Gly Pro Asp
435 440 445

Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro Gly Val Asn
 450 455 460

5 Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser
 465 470 475 480

Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu Leu Phe Ile
 485 490 495

10 Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys Gln Ala Asn
 500 505 510

Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr Ile Thr Val
 515 520 525

15 Ser Ala Glu Leu Pro Lys Pro Ser Ile Ser Ser Asn Asn Ser Lys Pro
 530 535 540

20 Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Ala Gln
 545 550 555 560

Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser
 565 570 575

25 Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn
 580 585 590

Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile Gln Asn Ser
 595 600 605

30 Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val Leu Tyr Gly
 610 615 620

35 Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr Leu Ser Gly
 625 630 635 640

Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro Ser Pro Gln
 645 650 655

40 Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr Gln Val Leu
 660 665 670

Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr Ala Cys Phe
 675 680 685

45 Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val Lys Ser Ile
 690 695 700

50 Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala Gly Ala Thr
 705 710 715 720

Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu Ile
 725 730

55 (2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

10 CCAGTGAATT CCTAATACGA CTACCTATAG GTTAAAACAG C

41

(2) INFORMATION FOR SEQ ID NO:19:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

25 GATGAACCT CGAGACCCAT TATG

24

(2) INFORMATION FOR SEQ ID NO:20:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCACCAAGTA CGTAACCACA TATGG

25

(2) INFORMATION FOR SEQ ID NO:21:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: cDNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTGAGGACTG CTGG

14

(2) INFORMATION FOR SEQ ID NO:22:

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: cDNA

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CACCACTGCC CTCGAGAAGC TCACTATTG

29

(2) INFORMATION FOR SEQ ID NO:23:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: cDNA

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CACCACTGCC CTCGAGAAGC TCACTATTG

29